



#9

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SEQUENCE LISTING

<110> HIATT, ANDREW C.
HEIN, MICH B.

<120> METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
PROTECTION PROTEINS IN PLANTS AND THEIR USE

<130> EPI3002E

<140> 09/982,107

<141> 2001-10-16

<160> 19

<170> PatentIn Ver. 2.1

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Gly	Asn	Gly	Thr	Phe	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr	Ser	Arg	Asp	
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Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys
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125 130 135 140	
aca aag gac ata ggc aga act gtg acc atc gaa tgc cgt ttc aaa gag	541
Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu	
145 150 155	
ggg aat gct cat agc aag aaa tcc ctg tgt aag aag aga gga gag gcc	589
Gly Asn Ala His Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala	
160 165 170	
tgc gaa gtt gtc atc gac tct act gag tac gtg gac ccc agc tat aag	637
Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys	
175 180 185	
gac aga gca atc ctt ttt atg aaa ggg acc agc cgc gat ata ttc tat	685
Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr	
190 195 200	
gtc aac att agc cac cta ata ccc agt gat gct gga ctg tat gtt tgc	733
Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys	
205 210 215 220	
caa gct gga gaa ggc ccc agt gct gat aaa aat aat gct gac ctc cag	781
Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln	
225 230 235	
gtg cta gag cct gag cca gag ctg ctt tat aaa gac ctg agg tcc tca	829
Val Leu Glu Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser	
240 245 250	
gtg act ttt gaa tgt gac ctg ggc cgt gaa gtg gca aat gat gcc aaa	877
Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys	
255 260 265	

tat ctg tgt cgg aag aac aag gaa acc tgt gat gtc atc atc aac acc	925
Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr	
270 275 280	
ctg ggg aag aga gat cca gcc ttt gaa ggc agg atc ctg cta acc ccc	973
Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro	
285 290 295 300	
agg gat gac aat ggc cgc ttc agt gtg ttg atc aca ggc ctg agg aag	1021
Arg Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys	
305 310 315	
gag gat gca ggg cac tac cag tgt gga gcg cac agt tct ggt ttg cct	1069
Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro	
320 325 330	
caa gaa ggc tgg ccc gtc cag gct tgg caa ctc ttt gtc aat gaa gag	1117
Gln Glu Gly Trp Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu	
335 340 345	
tcc acg att ccc aat agt cgc tct gtt gtg aag ggt gtc aca gga ggc	1165
Ser Thr Ile Pro Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly	
350 355 360	
tct gtg gcc atc gtc tgt ccc tat aac ccc aag gaa agc agc agc ctc	1213
Ser Val Ala Ile Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu	
365 370 375 380	
aag tac tgg tgt cac tgg gaa gcc gac gag aat gga cgc tgc ccg gtg	1261
Lys Tyr Trp Cys His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val	
385 390 395	
ctc gtg ggg acc cag gcc ctg gtg caa gaa gga tat gaa ggc cga ctg	1309
Leu Val Gly Thr Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu	
400 405 410	
gca ctg ttc gat cag ccg ggc agt ggc gcc tac act gtc atc ctc aac	1357
Ala Leu Phe Asp Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn	
415 420 425	
cag ctc acc acc cag gat tct ggc ttc tac tgg tgt ctt acc gat ggt	1405
Gln Leu Thr Thr Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly	
430 435 440	
gac tct cgc tgg aga acc acg ata gaa ctg cag gtt gct gaa gct aca	1453
Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr	
445 450 455 460	
aag aag cca gac ctt gag gtg aca cca cag aac gcg acc gcg gtg ata	1501
Lys Lys Pro Asp Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile	
465 470 475	
gga gag acc ttc aca atc tcc tgc cac tat ccg tgc aaa ttc tac tcc	1549
Gly Glu Thr Phe Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser	
480 485 490	

cag gag aaa tac tgg tgc aag tgg agc aac gac ggc tgc cac atc ctg	1597
Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu	
495 500 505	
ccg agc cat gat gaa ggt gcc cgc cag tcc tct gtg agc tgt gac cag	1645
Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln	
510 515 520	
agc agc cag atc gtc tcc atg acc ctg aac ccg gtc aaa aag gaa gat	1693
Ser Ser Gln Ile Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp	
525 530 535 540	
gaa ggc tgg tac tgg tgt ggg gta aaa gaa ggt cag gtc tat gga gaa	1741
Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu	
545 550 555	
act aca gcc atc tat gta gca gtt gaa gag agg acc aga ggg tca ccc	1789
Thr Thr Ala Ile Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro	
560 565 570	
cac atc aac ccg aca gat gca aac gca cgt gca aaa gat gct cca gag	1837
His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu	
575 580 585	
gaa gag gca atg gaa tcc tct gtc agg gag gat gaa aac aag gcc aat	1885
Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn	
590 595 600	
ctg gac ccc agg ctt ttt gca gac gaa aga gag ata cag aat gcg gga	1933
Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly	
605 610 615 620	
gac caa gct cag gag aac aga gca tct ggg aat gct ggc agt gct ggt	1981
Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly	
625 630 635	
gga caa agc ggg agc tcc aaa gtc cta ttc tcc acc ctg gtg ccc ctg	2029
Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu	
640 645 650	
ggt ttg gtg ctg gca gtg ggt gct gtg gct gtg tgg gtg gcc aga gtc	2077
Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val	
655 660 665	
cga cat cgg aag aat gta gac cgc atg tca atc agc agc tac agg aca	2125
Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr	
670 675 680	
gac att agc atg gga gac ttc agg aac tcc agg gat ttg gga ggc aat	2173
Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn	
685 690 695 700	
gac aac atg ggc gcc act cca gac aca caa gaa aca gtc ctc gaa gga	2221
Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly	
705 710 715	

aaa gat gaa ata gag act acc acc gag tgt acc acc gag cca gag gaa 2269
 Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu
 720 725 730

tcc aag aaa gca aaa agg tca tcc aag gag gaa gct gac atg gcc tac 2317
 Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr
 735 740 745

tca gca ttc ctg ttt cag tcc agc aca ata gct gcg cag gtc cat gat 2365
 Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp
 750 755 760

ggc ccc cag gaa gcc tag gcagtgtga ccacctacc ctgcctgtga 2413
 Gly Pro Gln Glu Ala
 765

caatcaactt gagaatcaca ttgatccact cgcagcccac cctcgcccat caccaggt 2473

cttccctcct gttctcagag gtgtgctggt tcctccctca gtcgtggaag cctggcctac 2533

ttatgcctgt ttaggagaga gcgtgaggag ttctttttgc tgttaaagag taaggtggaa 2593

atgagttgag cccaagaggt gtctctgaga gacgagggtt cagagcaggg gctcatttca 2653

ggaggaagag ccatttgaag cctctttata cacatatgct aggatgtcag gatagctctt 2713

ctcctccatc tctcctttct tctcttcttg attcagacaa cagatccgaa aactcactag 2773

gcttcgggtg tctactaaat gctgagagtc aggccacagc ctttctataa acatcactgg 2833

aagagacacc acctcgctcc agattctgtc ttttccttaa gctatcaatc attaccgggg 2893

attccctttg cctctgcacc tcataggcaa caaaagaaac ataagtcctg cagtctaagg 2953

catacccaag ccataagggc accacgagac tcagatgaga agagattttt ctccagagta 3013

ctcagtgaga tagactagt tcaagccaga tggggcaact cctggctctt ggccctgggac 3073

ttgtcttcaa gatctctgct cttattagag aaagaacttt agcatgagga aaagtaagag 3133

aaaacaagtt acatgggcat ggtgggtgtgc tcctgcaatc ccaatattaa gaggttaaaa 3193

aataggacca gaagtttaaa gtaatccttg gctacctagt gagtgttaagg ccagcctgga 3253

atcaataaga gttggt 3269

<210> 10

<211> 769

<212> PRT

<213> Rattus sp.

<400> 10

Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val
 1 5 10 15

Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu
 20 25 30

Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
 35 40 45
 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
 50 55 60
 Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
 65 70 75 80
 Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn
 85 90 95
 Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu
 100 105 110
 Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser
 115 120 125
 Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile
 130 135 140
 Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His
 145 150 155 160
 Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val
 165 170 175
 Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile
 180 185 190
 Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser
 195 200 205
 His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu
 210 215 220
 Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro
 225 230 235 240
 Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu
 245 250 255
 Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg
 260 265 270
 Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg
 275 280 285
 Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn
 290 295 300
 Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly
 305 310 315 320
 His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp
 325 330 335

Pro	Val	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ser	Thr	Ile	Pro	
			340						345			350				
Asn	Ser	Arg	Ser	Val	Val	Lys	Gly	Val	Thr	Gly	Gly	Ser	Val	Ala	Ile	
			355			360						365				
Val	Cys	Pro	Tyr	Asn	Pro	Lys	Glu	Ser	Ser	Ser	Leu	Lys	Tyr	Trp	Cys	
			370			375						380				
His	Trp	Glu	Ala	Asp	Glu	Asn	Gly	Arg	Cys	Pro	Val	Leu	Val	Gly	Thr	
385						390			395						400	
Gln	Ala	Leu	Val	Gln	Glu	Gly	Tyr	Glu	Gly	Arg	Leu	Ala	Leu	Phe	Asp	
			405						410			415				
Gln	Pro	Gly	Ser	Gly	Ala	Tyr	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr	Thr	
			420			425						430				
Gln	Asp	Ser	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asp	Gly	Asp	Ser	Arg	Trp	
			435			440						445				
Arg	Thr	Thr	Ile	Glu	Leu	Gln	Val	Ala	Glu	Ala	Thr	Lys	Lys	Pro	Asp	
450						455			460							
Leu	Glu	Val	Thr	Pro	Gln	Asn	Ala	Thr	Ala	Val	Ile	Gly	Glu	Thr	Phe	
465						470			475						480	
Thr	Ile	Ser	Cys	His	Tyr	Pro	Cys	Lys	Phe	Tyr	Ser	Gln	Glu	Lys	Tyr	
			485						490			495				
Trp	Cys	Lys	Trp	Ser	Asn	Asp	Gly	Cys	His	Ile	Leu	Pro	Ser	His	Asp	
			500			505						510				
Glu	Gly	Ala	Arg	Gln	Ser	Ser	Val	Ser	Cys	Asp	Gln	Ser	Ser	Gln	Ile	
			515			520						525				
Val	Ser	Met	Thr	Leu	Asn	Pro	Val	Lys	Lys	Glu	Asp	Glu	Gly	Trp	Tyr	
530						535			540							
Trp	Cys	Gly	Val	Lys	Glu	Gly	Gln	Val	Tyr	Gly	Glu	Thr	Thr	Ala	Ile	
545						550			555						560	
Tyr	Val	Ala	Val	Glu	Glu	Arg	Thr	Arg	Gly	Ser	Pro	His	Ile	Asn	Pro	
			565						570			575				
Thr	Asp	Ala	Asn	Ala	Arg	Ala	Lys	Asp	Ala	Pro	Glu	Glu	Glu	Ala	Met	
			580			585						590				
Glu	Ser	Ser	Val	Arg	Glu	Asp	Glu	Asn	Lys	Ala	Asn	Leu	Asp	Pro	Arg	
			595			600						605				
Leu	Phe	Ala	Asp	Glu	Arg	Glu	Ile	Gln	Asn	Ala	Gly	Asp	Gln	Ala	Gln	
610						615			620							
Glu	Asn	Arg	Ala	Ser	Gly	Asn	Ala	Gly	Ser	Ala	Gly	Gly	Gln	Ser	Gly	
625						630			635						640	

Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
645 650 655

Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
660 665 670

Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
675 680 685

Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
690 695 700

Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
705 710 715 720

Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
725 730 735

Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
740 745 750

Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
755 760 765

Ala

<210> 11
<211> 322
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Guy's 13 Kappa

<220>
<221> CDS
<222> (8)..(322)

<400> 11
ctcgagc gac att gtg atg acc cag tct cca gca atc atg tct gca tct 49
Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
1 5 10

cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt gta agt 97
Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
15 20 25 30

tac atg cac tgg ttc cag cag aag cca ggc act tct ccc aaa ctc tgg 145
Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp
35 40 45

ctt tat agc aca tcc aac ctg gct tct gga gtc cct gct cgc ttc agt 193
Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga atg gag 241
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu
 65 70 75

gct gaa gat gct gcc act tat tac tgc cat caa agg act agt tac ccg 289
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro
 80 85 90

tac acg ttc gga ggg ggg acc aag ctg gaa ata 322
 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 95 100 105

<210> 12
 <211> 105
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Guy's 13 Kappa

<400> 12
 Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15
 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30
 His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr
 35 40 45
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80
 Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105

<210> 13
 <211> 402
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Guy's 13 Gamma 1

<220>
 <221> CDS
 <222> (7)..(402)

<400> 13

ctcgag atg gaa tgg acc tgg gtt ttt ctc ttc ctc ctg tca gga act 48
 Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr
 1 5 10

gca ggc gtc cac tct ggg gtc cag ctt cag cag tca gga cct gac ctg 96
 Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
 15 20 25 30

gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga tac 144
 Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga aag 192
 Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys
 50 55 60

agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act tac 240
 Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr
 65 70 75

tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat tcc 288
 Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser
 80 85 90

tcc acc tca gcc tac atg gag ctc cgc agc ctg aca tct gag gac tct 336
 Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
 95 100 105 110

gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc acc 384
 Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

act ctc aca gtc tcc tca 402
 Thr Leu Thr Val Ser Ser
 130

<210> 14

<211> 132

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Guy's 13 Gamma 1

<400> 14

Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15

Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
 50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
 85 90 95
 Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 115 120 125
 Thr Val Ser Ser
 130

<210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
 accagatcta tggaatggac ctgggttttt c

31

<210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 16
 cccaagcttg gttttggaga tggttttctc

30

<210> 17
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 17
 gataagcttg gtctactcc tcctcctcct a

31

<210> 18
 <211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
aatctcgagt cagtagcaga tgccatctcc

30

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
ggaaagcttt gtacatatgc aaggcttaca

30